

IDENTIFICATION

Species: *Lactuca sativa*

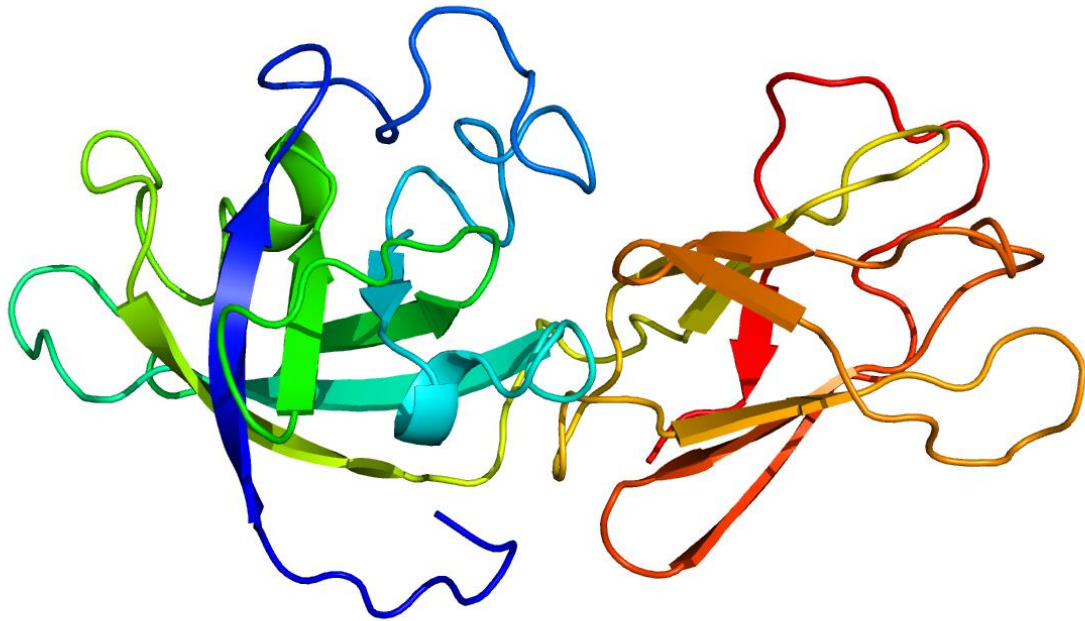
Locus: Lsat_1_v5_gn_9_23601

Gene Model: Lsat_1_v5_gn_9_23601.3

Description: LsEXPA-31

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Lsativa_V8

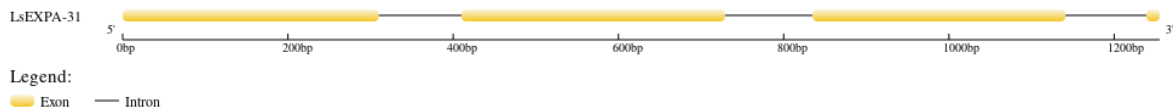
KEGG: <https://www.genome.jp/entry/T05352>

EXTERNAL RESOURCES

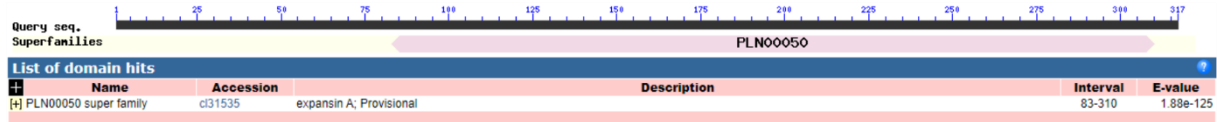
<https://lgr.genomecenter.ucdavis.edu/>

<https://www.lettucegdb.com/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>LsEXPA-31

LTSRYFYNIHPNRLHKYQHNYLPFLHIPTINFPHPLSPNPTEELRSALLCRTDMGLAGG
ILFIIVTISVFSATHARIPGNYAGGSWQGAHATFYGGSDASGTMGGACGYGNLYSQG
YGVNTAALSTALFNKGFSCGACFEIKCSQDPRWCHPGSPSIFITATNFCPPNFALPNDN
GGWCNPPRTHFDLAMPMLKIAEYRAGIVPVSYRRVPCRKAGGIRFTINGHRYFNLIL
ISNVAGAGDVQKVWVKGTKTNWMSMSRNWQNWQSNVVLVGQALSFRVTGSDR
RTSTSWNIAPASWQFGQFTTGKNFRVGFKS*

CDS (coding sequence)

>LsEXPA-31

CTTACAAGTCGTTACTTTTATAACATCCACCCGAATCGCCTCCATAAATACCAGCA
TAACTACCTCCCATTTCTTCACATTCCCACCATTAACCTCCCTCACCTCTCTCTCC
GAACCAACTGAAGAGCTCAGATCTGCTCTCTTGTCGGGACTGACATGGGTCTC
GCCGGCGGCATTCTCTTCATCATCGTCACCATCTCGGTTTTCTCAGCGACCCACGC
CAGAATCCCTGGAACTACGCCGGCGGCTCGTGGCAAGGTGCTCATGCTACCTTC
TATGGTGGCAGTGACGCCTCTGGCACTATGGGAGGTGCTTGTGGTTATGGAAACC
TGTACAGCCAAGGCTACGGCGTTAACACGGCGGCGCTGAGCACGGCGTTGTTCAA
CAAAGGGTTTAGCTGCGGTGCGTGCTTCGAAATCAAGTGCAGCCAAGATCCGAG
GTGGTGCCATCCCGGCAGCCCCTCCATCTTCATCACCGCCACTA ACTTCTGCCCTC
CGAACTTCGCTCTCCCTAACGACAATGGTGGATGGTGTAAACCCTCCTCGTACCCA
CTTCGACCTCGCCATGCCCATGTTCTCAAGATCGCCGAATACCGCGCCGGAATC
GTCCCCGTTTCTTATCGCCGAGTGCCATGCCGGAAGCTGGTGGGATCAGGTTCA
CCATCAACGGCCACCGTTACTTCAACTTGATTTTAATCAGCAACGTCGCGGGTGC
AGGGGATGTCCAGAAGGTCTGGGTCAAAGGGACGAAAATAATTGGATGAGCAT
GAGTCGTA ACTGGGGTCAA AATTGGCAGTCAAACGCCGTCTCGTCCGGTCAAGCA
CTCTCCTTCAGGGTCACCGGGAGTGACCGGCGAACCTCCACCTCATGGAACATCG
CTCCGGCGAGTTGGCAGTTTGGTCAAACCTTCACCGGAAAGAATTTCCGAGTGGG
CTTCAA AAGCTAA

Nucleotide

>LsEXPA-31

CTTACAAGTCGTTACTTTTATAACATCCACCCGAATCGCCTCCATAAATACCAGCA
TAACTACCTCCCATTTCTTCACATTCCCACCATTAACTTCCCTCACCTCTCTCTCC
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GCCGGCGGCATTCTCTTCATCATCGTCACCATCTCGGTTTTCTCAGCGACCCACGC
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GCTACGGCGTTAACACGGCGGCGCTGAGCACGGCGTTGTTCAACAAAGGGTTTAG
CTGCGGTGCGTGCTTCGAAATCAAGTGCAGCCAAGATCCGAGGTGGTGCCATCCC
GGCAGCCCCCTCCATCTTCATCACCGCCACTAACTTCTGCCCTCCGAACTTCGCTCT
CCCTAACGACAATGGTGGATGGTGTAAACCCTCCTCGTACCCACTTCGACCTCGCC
ATGCCCATGTTCTCAAGATCGCCGAATACCGCGCCGGAATCGTCCCCGTTTCTTA
TCGCCGGTAAATTTACACATATCCATTCTCTGTTTCTAAAAACACCTGCATTGCGT
GATATTTCTGAGGAAATGACGAAACTGACCTTGGTGTCTGTGATGTATTACTACA
GAGTGCCATGCCGGAAGCTGGTGGGATCAGGTTACCATCAACGGCCACCGTTA
CTTCAACTTGATTTTAATCAGCAACGTCGCGGGTGCAGGGGATGTCCAGAAGGTC
TGGGTCAAAGGGACGAAAATAATTGGATGAGCATGAGTCGTAACCTGGGGTCAA
AATTGGCAGTCAAACGCCGTCCTCGTCGGTCAAGCACTCTCCTTCAGGGTCACCG
GGAGTGACCGGCGAACCTCCACCTCATGGAACATCGCTCCGGCGAGTTGGCAGTT
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